

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher: pruluki

Searcher Phone #: _____

Searcher Location: _____

Date Searcher Picked Up: 8/15Date Completed: 8/30

Searcher Prep & Review Time: _____

Clencal Prep Time: _____

Online Time: _____

Type of Search

NA Sequence (#) _____

AA Sequence (#) _____

Structure (#) _____

Bibliographic _____

Litigation _____

Fulltext _____

Patent Family _____

Other _____

Vendors and cost where applicable

STN _____

Dialog _____

Questel Orbit _____

Dr. Link _____

Lexis/Nexis ok

Sequence Systems _____

WWW/Internet _____

Other (specify) _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 29, 2001, 21:07:53 ; Search time 1467.33 Seconds
(without alignments)
7684.699 Million cell updates/sec

Title: US-09-684-725-1
Perfect score: 729
Sequence: 1 atggaataacttcagaatgc.....cactcagagtgcagtatctag 729

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank: *
1: gb_ba1: *
2: gb_ba2: *
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4: gb_in1: *
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8: gb_ov: *
9: gb_pat1: *
10: gb_pat2: *
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92: gb_pr8: *
93: gb_pr9: *
94: gb_r01: *
95: gb_r02: *
96: gb_in4: *
97: gb_pr10: *
98: em_ba3: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	729	100.0	216673	60	AC008571 Homo sapi
2	717.8	98.5	1239	89	AF242874 Homo sapi
3	717.8	98.5	1248	85	AB041228 Homo sapi
4	717.8	98.5	1298	85	AF272363 Homo sapi
5	716.2	98.2	1248	89	AF292402 Homo sapi
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7	471.4	64.7	1314	94	AB041229 Homo sapi
8	280.8	38.5	828	93	HS06PCR1 Homo sapi

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9 280.8 38.5 1318 89 AF272362 Homo sapi
10 280.8 38.5 187451 64 AC017104 Homo sapi
11 255 1209 94 AF242873 Rattus no
12 255 1239 94 AB038649 Rattus no
13 243 1218 94 AF044602 Mus muscu
14 159.6 21.9 75950 74 AC073449 Homo sapi
15 134.8 18.5 2040 88 AF034632 Homo sapi
16 134.8 18.5 163284 89 AF037000 Human DNA
17 133.2 17.4 1254 45 AF082210 Spheroioid
18 127 17.4 4131 93 HSNENRA E11480 cDNA encodi
19 127 17.4 4131 93 HSNENRA X70070 H. sapiens m
20 120.4 16.5 870 97 HSN60181 U60181 Human growt
21 120.4 16.5 1101 97 HSN60179 AC069523 Homo sapi
22 120.4 16.4 121552 60 AC008191 AC008191 Drosophi
23 119.8 16.4 140838 65 AC007441 AC007441 Drosophi
24 119.8 16.4 219832 60 AC003703 AE003703 Drosophi
25 119.8 16.4 225374 5 AE003703 AE003703 Drosophi
26 118.8 16.3 150566 64 AC016938 AC016938 Homo sapi
27 118.8 15.6 870 7 SS060180 U60180 Sus scrofa
28 114 15.6 1101 7 SS060178 U60178 Sus scrofa
29 114 15.4 1161 10 I15508 I15508 Sequence 2
30 112.4 15.4 1161 10 I15508 I15508 Sequence 2
31 112.4 15.4 1370 10 I20930 I20930 Sequence 1
32 112.4 15.4 1370 10 I20930 I20930 Sequence 1
33 112.4 15.4 1370 10 I20930 I20930 Sequence 1
34 112.4 15.4 1466 10 I20931 I20931 Sequence 3
35 112.4 15.4 1466 10 I20931 I20931 Sequence 3
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38 112.4 15.4 1510 10 I20932 I20932 Sequence 5
39 110 15.1 1529 95 RNNR2RBC X97121 R. norvegicu
40 109.2 15.0 1350 94 AB001982 AB001982 Rattus norv
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42 106.6 14.6 3947 94 AB017027 AB017027 Mus muscu
43 101.6 13.9 2379 7 BTD2DOR X51657 B. taurus do
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ALIGNMENTS

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RESULT 1 AC008571 216673 bp DNA HTG 05-MAY-2000
LOCUS AC008571/c Homo sapiens chromosome 5 clone CTC-550M4, WORKING DRAFT SEQUENCE.
DEFINITION 9 unordered pieces.
ACCESSION AC008571.3 GI:7708957
VERSION AC008571.3
WORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 216673)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 216673)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On May 5, 2000 this sequence version replaced gi:7211884.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 396672, H361
Center clone name: CIT-HSPC_550M4
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Summary Statistics
Consensus quality: 197198 bases at least Q40
Consensus quality: 207925 bases at least Q30
Consensus quality: 210803 bases at least Q20
Estimated insert size: 223000; pulse field gel estimation
Estimated insert size: 215873; sum-of-contigs estimation
Quality coverage: 5.46 in Q20 bases; pulse field gel estimation
Quality coverage: 5.64 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 9 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
be preserved.

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1 3049 3148: contig of 3048 bp in length
* 3049 3148: contig of 3048 bp in length
* 3149 3149: contig of 5257 bp in length
* 8406 8406: gap of unknown length
* 8506 8506: gap of unknown length
* 23493 23492: contig of 14987 bp in length
* 23593 23592: gap of unknown length
* 40019 40018: contig of 16426 bp in length
* 40119 40118: gap of unknown length
* 54776 54776: contig of 14658 bp in length
* 54877 54876: gap of unknown length
* 80051 80050: contig of 25174 bp in length
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* 12105 12104: gap of unknown length
* 121205 121204: gap of unknown length
* 167092 167091: contig of 45887 bp in length
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BASE COUNT 66753 a 41883 c 42226 g 65000 t 811 others
ORIGIN

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Query Match 100.0%; Score 729; DB 60; Length 216673;
Best Local Similarity 100.0%; Pred. No. 4e-130;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 ccttcagcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 300
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QY 301 tatgagatgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 360
DB 84103 TATGAGATGTGCGGCACTACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 84044
QY 361 gccctcttgagacgctgtgtctgctcctcctcctcctcctcctcctcctcctcctcct 420

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Db	83983	C CCTACG76GCATCCTTACACCCTGTTCCGCGCAAACATGCAAGAACACCGGCGCGGCC	83924
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DEFINITION	Homo sapiens neuromedin u receptor 2 (NMU2R) mRNA, complete cds.		
VERSION	AF242874		
KEYWORDS	AF242874.1 GI:9082155		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1239) Howard,A.D., Wang,R., Pong,S.S., Mellin,T.N., Strack,A., Guan,X.M., Zeng,Z., Williams,D.L. Jr., Reighner,S.D., Nunes,C.N., Murphy,B., Stall,J.N., Yu,H., Jiang,Q., Clements,M.K., Tan,C.P., McKee,K.K., Henrik,D.L., McDonald,T.P., Lynch,K.R., Evans,J.F., Austin,C.P., Caskey,C.T., Van der Ploeg,L.H. and Liu,Q. Identification of receptors for neuromedin U and its role in feeding Nature 406 (6791), 70-74 (2000)		
JOURNAL MEDLINE	20351041		
REFERENCE	2 (bases 1 to 1239)		
AUTHORS	Liu,Q., McDonald,T.P., Wang,R., Jiang,Q. and Howard,A.D.		
JOURNAL TITLE	Direct Submission		
Submitted (09-MAR-2000)	Pharmacology, Merck Research Labs, West Point, PA 19486, USA		
FEATURES			
source	Location/Qualifiers		
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BASE COUNT	267 a	392 c	265 g	315 t					
ORIGIN									
Query Match	98.5%	Score 717.8:	DB:89;	Length 1239;					
Best Local Similarity	99.7%	Pred. No. 1.9e-127;							
Matches 719:	Conservative	0:	Mismatches	2:	Indels	0:	Gaps	0:	
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Dd	1	ATGGAAAAACTTCAGAAATGCTTCCTGGATCTACAGCAAGAAACTAGAAATCATTCCAG	60						
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Dd	61	AAACACCTGAACAGCAGCCGAGAGATATGTGGCTTCCCTCCGCGACCTCCGCGCAGCCAC	120						
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Dd	241	CTCTTCAACCTCGGCGGTCTCTACCTCCTGTGCTCCGTGCTCTTGGATCCCTCTGAAGGTC	300						
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Dd	301	TATGAGATGTGGCGCACTACCCCTTCTTGTGTCGGGGCCGTTGGGCTGCTACTTCAAGACG	360						
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Dd	361	GCCCTCTTGTGAACACGCTGTGCTCCCTCCATCCACATCACACACCGTCAAGCTTGAG	420						
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Dd	541	ATCCATGGCATCAATCTCCACTACTTCCCAATGGGTCCTGTGTCCAGAGTTGGCCACCC	600						
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Dd	721 A	721 A 721							
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LOCUS									
DEFINITION	Homo sapiens mRNA for G protein-coupled receptor TGR-1, complete cds.								
ACCESSION	AB041228								
VERSION	AB041228.1 GI:10257380								
KEYWORDS	G protein-coupled receptor TGR-1.								
SOURCE	Homo sapiens cDNA to mRNA.								

Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo. 1 (sites). Hosoya, M., Moriya, T., Kawamata, Y., Ohkubo, S., Fujii, R., Matsui, H., Shirahata, Y., Fukusuma, S., Habata, Y., Hinuma, S., Onda, H., Nishimura, O. and Fujino, M. Identification and Functional Characterization of a Novel Subtype of Neuregulin 1 Receptor. *J. Biol. Chem.* 275 (38), 29528-29532 (2000) 10887190 2 (bases; 1 to 1248) Shirahata, Y., Moriya, T., Ohkubo, S. and Matsui, H. Direct Submission Submitted (03-APR-2000) to the DDBJ/EMBL/Genbank databases. Yasushihara, T., Takeda Chemical Industries, LTD, Discovery Research Laboratories 1, 10 Wadai, Tsukuba, Ibaraki 300-8293, Japan (E-mail: Shirahata.Yasushihara@takeda.co.jp, Tel: 81-298-64-5011, Fax: 81-298-64-5000)

gene	10. .1248
CDS	10. .1248

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Best Local Similarity	99.7%;	Pred. No. 1.9e-127;		
Matches 719; Conservative	0;	Mismatches 3;	Indels 0;	

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Db	430	GGCTACGTGGGCATCTCTACACC CGTTCCGGCCAAACTGCAGAGCACC GGCGGGCC	489
Oy	481	ctcaagatccctggagcatcgtctctgggaccttccgtctcttctccctgccaaacacagc	540
Db	480	CTCAGGATCTCGGCGCATGCTGTGGGGCTCTCCGCTGCTCTCTCTCCCTGCCAACACAGC	549
Oy	541	atccaatggcalcaagtctccactacttcccccaatagggtccctggtcccaagttcggaacc	600
Db	550	ATCCATGGCATCAAGTTCCTCCACTCTTCCCCAATGGGTCTCTGTCACAGTTCGGCCACC	609
Oy	601	tgtacggtlcatcaagcccatgltgatctataattcatcatcacaagttacaccttctcta	660
Db	610	TGTACGGTCTCATCAAGCCCATGTTGATCTCTCATATTTCATCATTCACAGTACCTCTTCTTA	669
Oy	661	tttaacctctcccaatgactgactgcatcatcaagtctctctactactcatcgaatcagaagt	720
Db	670	TTTCACTCTCTCCCCCAATGAGCTGTCTCATAGTGTCTCTCTACTCTCTCTCTCTCTCTCT	729
Oy	721	a 721	
Db	730	A 730	
RESULT	4		
LOCUS	AF272363		
DEFINITION	AF272363	1298 bp mRNA	PRI
ACCESSION	AF272363	Homo sapiens neuromedin U receptor 2 (NMUR2) mRNA, complete cds.	23-OCT-2000
VERSION	AF272363.1	GI:10946202	
KEYWORDS			
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE		1 (bases 1 to 1298)	
JOURNAL		Raddatz,R., Wilson,A.E., Arlymyshyn,R., Bonini,J.A., Borowsky,B.,	
REFERENCE		Boteju,L.W., Zhou,S., Kouranova,E.V., Nagorny,R., Guevarra,M.S.,	
AUTHORS		Daï,M., Lerman,G.S., Vayse,P.J., Brancheck,T.A., Gerald,C.,	
TITLE		Forray,C. and Adham,N.	
JOURNAL		Identification and Characterization of Two Neuromedin U Receptors	
REFERENCE		Differentially Expressed In Peripheral Tissues and the Central	
AUTHORS		Nervous System	
TITLE		J. Biol. Chem. 275 (42), 32452-32459 (2000)	
JOURNAL		U. Biol. Chem. 275 (42), 32452-32459 (2000)	
REFERENCE		10899166	
AUTHORS		2 (bases 1 to 1298)	
TITLE		Bonini,J.A., Raddatz,R., Wilson,A. and Borowsky,B.	
JOURNAL		Direct Submission	
REFERENCE		Submitted (23-MAY-2000) Target Discovery and Assessment, Synaptic	
AUTHORS		Pharmaceutical Corporation, 215 College Road, Paramus, NY 07652,	
TITLE		USA	
FEATURES			
Location/Qualifiers			

VTSELFLLPMTVISLVLYLMALRLKKDKSLEADENANIORPCRKSVNKMFLVLV
FAICWAPPHIDLPFSFVMESESLEAVNIVHYGVFVLSAVNPIYILSRF
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BASE COUNT 278 a 405 c 282 g 333 t
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Query Match 98.5%; Score 717.8; DB 89; Length 1298;
Best Local Similarity 99.7%; Pred. No. 1.9e-127;
Matches 719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db AAACACCTGAACAGCACAGAGAGATATGAGCTTCTCTGCGAGCCTCGGCGCACGCCAC 155
121 tcttccctcccgctgctgtgtgtatgtgtcaattcttggtgtgggttcattgtgcaat 180
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Db TTCTTCTCTCCCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 215
181 gtccctgt 240
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Db GTCTGT 275
216 gtccctgt 275
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Db CTTCTTGT 335
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Qy 301 tatgagaatgtgagcgaac 360
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336 gtccctcttgagacagctgt 420
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Db GCCCTTTTGAAGACGCTGT 455
396 gtccctcttgagacagctgt 455
Qy 421 cgtctagctgtgcatctctac 480
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Db CGCTAGTGTGGCATCTCTACACCGGTTCGCCGCAACCTCAGAGCACCGCGCGCGCGGC 515
456 cgtctagctgtgcatctctac 515
Qy 481 ctcaagatctctgagacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
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Db CTCAGATCTCTGGCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 575
516 ctcaagatctctgagacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 575
Qy 541 atccatgtgacatcaagcttccactacttcccaatgggttccctgtgtgtgtgtgtgtgt 600
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Db ATCCATGTGACATCAAGTTCACACTTCCCAATGGGTTCCTGTGTGTGTGTGTGTGTGT 635
576 atccatgtgacatcaagcttccactacttcccaatgggttccctgtgtgtgtgtgtgtgt 635
Qy 601 tgaagcgtcataagccatgt 660
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Db TGAAGCGTATCAAGCCATGT 695
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Qy 661 tttctactctctcccaatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
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696 tttctactctctcccaatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 755
Qy 721 a 721
Db 756 A 756

RESULT 5
AF292402 1248 bp mRNA PRI 11-DEC-2000
LOCUS AF292402 Homo sapiens neuromedin U receptor-type 2 mRNA, complete cds.
DEFINITION AF292402
ACCESSION AF292402
VERSION AF292402.1 GI:9944989
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1248)
AUTHORS Shan, L., Qiao, X., Crona, J. H., Behn, J., Wang, S., Laz, T., Bayne, M.,
Gustafson, E. L., Monsma, F. J., Jr. and Hedrick, J. A.
TITLE Identification of a Novel Neuromedin U Receptor Subtype Expressed
in the Central Nervous System
J. Biol. Chem. 275 (50), 39482-39486 (2000)
JOURNAL 11010960
PUBMED 2 (bases 1 to 1248)
REFERENCE Pang, L., Wang, S., Laz, T. and Hedrick, J. A.
AUTHORS Direct Submission
TITLE Submitted (02-AUG-2000) Human Genome Research, Schering-Plough
JOURNAL Research Institute, 2015 Galloping Hill Road, Kenilworth, NJ 07033,
USA

FEATURES
source Location/Qualifiers
1..1248
/organism="Homo sapiens"
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/chromosome="5"
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/note="G protein coupled receptor; Nmu-R2"
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/product="neuromedin U receptor-type 2"
/protein_id="AAG03064.1"
/db_xref="GI:9944989"

CDS

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ORIGIN

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Best Local Similarity 99.6%; Pred. No. 3.9e-127;
Matches 718; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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61 aaacacctgaacagacacagagagatcttgccctccctctgagacctcgagcgagccac 120
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Db AAACACCTGAACAGCACAGAGAGATATGAGCTTCTCTGCGAGCCTCGGCGCACGCCAC 129
70 aaacacctgaacagacacagagagatcttgccctccctctgagacctcgagcgagccac 129
Qy 121 tcttccctcccgctgctgt 180
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Db TTCTTCTCTCCCGT 189
130 tcttccctcccgctgctgt 189
Qy 181 gtccctgt 240
|||||
Db GTCTGT 249
190 gtccctgt 249
Qy 241 cctctcaagccttgagctgt 300
|||||
Db CTTCTAGCCTGTGGCGGT 309
250 cttctcaagccttgagctgt 309
Qy 301 tatgagaatgtgagcgaac 360
|||||
Db TATGAGATGTGGCGCACTACCTTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 369
310 tatgagaatgtgagcgaac 369
Qy 361 gtccctcttgagacagctgt 420
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Db GCCCTTTTGAAGACGCTGT 429
370 gtccctcttgagacagctgt 429
Qy 421 cgtctagctgtgcatctctac 480
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Db 430 CGTACGTGGCCATCTACACCCGTTCCGGCCAACTGCAGAGACCCGGCGCGGCG 489
 QY 481 ctcaagatcctcggcagcagctcgtgagctctcgtctctcctccgccaacacagc 540
 Db 490 CTCAGATCCCTCGGCATCGTCTGGGGCTTCCGCTCTTCCCTGCGCCACACCGC 549
 QY 541 atccatggcatcaagttccactactctcccaatgggtccctgggtcccaagttcgccac 600
 Db 550 ATCCATGGCATCAAGTTCCTACTCTCCCAATGGGTCTCCGTGCTCCAGGTTGGCGCAC 609
 QY 601 tctacgtcatcaagccatgtagatctacatctatcatcaagtcactctctccta 660
 Db 610 TGTACGGTCAATCAAGCCCATGTGATCTACAAATTTTCATCAATCCAGGTCACCTCTTCTTA 669
 QY 661 tttactctctcccatgtagatctcatcaagttctcctactactactcagtcagtcagagtg 720
 Db 670 TTTCTACTCTCTCCCATGATCTCATACAGTGTCTCTCTACTACTCATGACATCACTA 729
 QY 721 a 721
 Db 730 A 730

RESULT 6
 AF242875 LOCUS AF242875 1188 bp mRNA ROD 13-JUL-2000
 DEFINITION Rattus norvegicus neuromedin U receptor 2 (NMU2R) mRNA, complete
 ACCESSION AF242875
 VERSION AF242875.1 GI:9082157
 KEYWORDS Norway rat.
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 1188)
 HOWARD,A.D., Wang,R., Pong,S.S., Mellin,T.N., Strack,A., Guan,X.M.,
 Zeng,Z., Williams,D.L., Jr., Reighner,S.D., Nunes,C.N., Murphy,B.,
 Stiel,J.N., Yu,H., Jiang,Q., Clements,M.K., Tan,C.P., McKee,K.K.,
 Hreniak,D.L., McDonald,T.P., Lynch,K.R., Evans,J.F., Austin,C.P.,
 Caskey,C.T., Van der Ploeg,L.H. and Liu,Q.
 Identification of receptors for neuromedin U and its role in
 feeding
 JOURNAL Nature 406 (6791), 70-74 (2000)
 MEDLINE 20351041
 REFERENCE 2 (bases 1 to 1188)
 AUTHORS Liu,Q., McDonald,T.P., Wang,R., Jiang,Q. and Howard,A.D.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2000) Pharmacology, Merck Research Labs, West
 Point, PA 19486, USA
 FEATURES
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 1. 1188
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
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 /protein_id="AF82756.1"
 /db_xref="GI:9082158"

/translation="MGKLEASVTHPIPLMKYLNSTSEYLAHLGPKRSDLSPLSVAY
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 PLFGVGCFTKALFEYVCFASILSVTVSVYVAIVHPRAKLESTRRLRLIS
 LWSFSVNSLPNTSIHGKIFQHPFNGSSVPSACVTVKPMVYNLLIIOAIFLEYI
 LPMTLISVLYLMGLRKRDSELEANKVAVNVIHPSRKSVTKMLVLYVYKICPTP
 HVDRLPFSEVTESTLAVPNLIHVYSGVFPYLSAVNPITYNLSRFRARFNV
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BASE COUNT 243 a 361 c 278 g 306 t
 ORIGIN

Query Match 64.7%; Score 471.4; DB 94; Length 1188;
 Best Local Similarity 79.8%; Pred. No. 1.9e-80;
 Matches 575; Conservative 0; Mismatches 131; Indels 15; Gaps 1;

QY 1 atggaanaactcagaatgtcttcctgagatctcaccagagaacatagaatcctcag 60
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 QY 61 aaacacccagacagaccggaagatattctgctctctctctgagacctcggcagacc 120
 Db 46 AAGTACTTGAACAGCAGAGAGAGATCTTGGCCACCTGTGTGAGACCCAGCGCAGTAC 105
 QY 121 tctctcccccgtgtcgtgtgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat 180
 Db 106 CTATCCCTTCCGGGT 165
 QY 181 gtccgtgtgtcctcgtgtgtatctctcagacacagacgtatgaagacgcccactactac 240
 Db 166 CTTGT 225
 QY 241 ctctcagacccgtgcgtctcgtctcgtctcgtctcgtctcgtctcgtctcgtctcgtctcgt 300
 Db 226 CTTTTCAGCTTGGCAGTCTGATGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 285
 QY 301 tatgaatgtgtgcgaactacaccttctgttctgcggccgtgtgtgtgtgtgtgtgtgtgt 360
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 QY 361 gccctcttgagaccgt 420
 Db 346 GCCCTTTCAGAGCTGT 405
 QY 421 cgtacgtgtgcacatctcaccacccgttccgcgccaactgtgagacccggtgcggcgcc 480
 Db 406 CGCATGTGCGCATTTGTGTCACACCTTTCGAGCCAGCACTGTGAGACGCGGCGGCGCC 465
 QY 481 ctaagatctcgtgacatgt 540
 Db 466 CTGAGGATCTTCAGACCTGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 525
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 Db 586 TGCACAGTCACCAACCCATGTGGGTGTATTAATTGATCATCAAGCTACAGCTTCCGC 645
 QY 661 tttactctctcccatgtagatctcatcaagttctcctactactactatgagtcagagtg 720
 Db 646 TTTTATATCTCTCCCATGATGACCTCATACAGCTCTTACTACTCATGAGGCTCAGGCTG 705
 QY 721 a 721
 Db 706 A 706

RESULT 7
 AB041229 LOCUS AB041229 1314 bp mRNA ROD 21-SEP-2000
 DEFINITION Rattus norvegicus mRNA for G protein-coupled receptor TGR-1,
 complete cds.
 ACCESSION AB041229
 VERSION AB041229.1 GI:10257382
 KEYWORDS G protein-coupled receptor TGR-1.
 Rattus norvegicus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (sites)
 AUTHORS Hosoya, M., Moriya, T., Kawamata, Y., Ohkubo, S., Fujii, R., Matsui, H., Shintani, Y., Fukusumi, S., Habata, Y., Hinuma, S., Onda, H., Nishimura, O. and Fujino, M.
 TITLE Identification and Functional Characterization of a Novel Subtype of Neuregulin U Receptor
 JOURNAL J. Biol. Chem. 275 (38), 29528-29532 (2000)
 PUBMED 10887190
 REFERENCE 2 (bases 1 to 1314)
 AUTHORS Fujii, R., Shintani, Y. and Hinuma, S.
 TITLE Direct Submission
 JOURNAL Submitted (03-APR-2000) to the DDBJ/EMBL/GenBank databases. Shuji Hinuma, Takeda Chemical Industries, LTD, Discovery Research Laboratories 1, Medai 10, Tsukuba, Ibaraki 300-4293, Japan (E-mail: Hinuma_Shuji@takeda.co.jp, Tel: 81-298-64-5035, Fax: 81-298-64-5000)
 FEATURES
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 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
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 CDS 127..1314
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 /db_xref="GI:10257383"
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 BASE COUNT 269 a 397 c 305 g 343 t
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 Query Match 64.7%; Score 471.4; DB 94; Length 1314;
 Best Local Similarity 79.8%; Pred. No. 1.9e-80;
 Matches 575; Conservative 0; Mismatches 131; Indels 15; Gaps 1;
 QY 1 atggaataactcaagaatcttccttgatcaccagcaagaataagaatccatccag 60
 Db 127 ATGGAAACTTGAAATGCTTCCTGATCCAC-----GATCCATCATG 171
 QY 61 aaacacctgaacagacagagagatctgagctctctgagagactcgagagacac 120
 Db 172 AAGTACTTGACACGACAGAGAGACTCTGGCCACCTGTGTGACCAAGCCAGTGAC 231
 QY 121 tctctcccccgtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
 Db 232 CTATCCCTTCGGGT 291
 QY 181 gtccagtggt 240
 Db 292 CTTCTGT 351
 QY 241 ctcttaagcgtgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
 Db 352 CTCTTACGCTTGAGCTGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 411
 QY 301 tatgagatgt 360
 Db 412 TACGAGATGTGACCAATTAACCTTTCCTGTGTGTGTGTGTGTGTGTGTGTGT 471
 QY 361 ggcctcttgagagcgt 420
 Db 472 GCCCTCTTGAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 531

QY 421 cgctacgtgagccatccctacacccggtccgcgcaaaactgagagacaccgagcgagcc 480
 Db 532 CGCTATGTGGCCATTGTGTCACACCTTTCCGAGCCAGCTGAGAGCACGCGCCACGCGCC 591
 QY 481 ctcaagatccctggcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
 Db 592 CTCAGATCCTCAGCCCTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 651
 QY 541 atccatgtgcaatgaatccactactccccaatgagtggtccctgtgtccaggtgtgcacc 600
 Db 652 ATCCATGTGCAATGAATGCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 711
 QY 601 tftacgtgtacaaagccagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
 Db 712 TGCAAGTGTACCAACCCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 771
 QY 661 tctaccctcccccactgtactgtactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
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 QY 721 a 721
 Db 832 A 832
 RESULT 8
 HSOGPCR1 HSOGPCR1 828 bp DNA PRI 22-JUL-1999
 LOCUS Homo sapiens orphan G protein-coupled receptor gene, first coding
 DEFINITION exon.
 ACCESSION AF044600
 VERSION AF044600.1 GI:2865467
 KEYWORDS
 SEGMENT
 SOURCE 1 of 2
 human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 828)
 AUTHORS Tan, C.P., McKee, K.K., Liu, Q., Palyha, O.C., Feigliner, S.D., Hreniuk, D.L.,
 TITLE Cloning and characterization of a human and murine T-cell orphan
 G-protein-coupled receptor similar to the growth hormone
 secretagogue and neurotensin receptors
 JOURNAL Genomics 52 (2), 223-229 (1998)
 MEDLINE 99000845
 PUBMED 9782091
 REFERENCE 2 (bases 1 to 828)
 AUTHORS Tan, C.T., McKee, K.K., Palyha, O.C., Feigliner, S.D., Hreniuk, D.L.,
 TITLE Direct Submission
 JOURNAL Submitted (16-JAN-1998) Biochemistry and Physiology, Merck and Co.
 Inc., P.O. Box 2000, Rahway, NJ 07065, USA
 FEATURES
 source Location/Qualifiers
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 BASE COUNT 134 a 267 c 256 g 171 t
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 Best Local Similarity 65.8%; Pred. No. 4.6e-44;
 Matches 408; Conservative 0; Mismatches 212; Indels 0; Gaps 0;
 QY 103 ggaacccggagcagcagcactctctcccggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 162
 Db 88 GGGCCCGAGCAGACAGAGCGCTTCAATGCGCCATGTGCGCCACATACCTGCTGATCTTCGTG 147
 QY 163 gtgggggtcaatgtgcaatgt 222
 Db 163 gtgggggtcaatgtgcaatgt 222

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Best Local Similarity	65.8%;	Pred. No. 4.1e-44;		
Matches 408; Conservative	0;	Mismatches 212;	Indels 0;	Gaps 0;

RESULT	10			
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LOCUS	AC017104	187451 bp	DNA	16-MAR-2001
DEFINITION	Homo sapiens chromosome 2 clone RP11-55215, WORKING DRAFT SEQUENCE.			

ACCESSION	10. unordered pieces.
VERSION	AC017104
KEYWORDS	AC017104.6 GI:13357551
SOURCE	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	1 (bases 1 to 187451)
REFERENCE	Waterston, R.H.
AUTHORS	The sequence of Homo sapiens clone
TITLE	unpublished
JOURNAL	2 (bases 1 to 187451)
REFERENCE	Waterston, R.H.
AUTHORS	Direct Submission
TITLE	Submitted (09-DEC-1999) Genome Sequencing Center, Washington
JOURNAL	University School of Medicine, 4444 Forest Park Parkway, St. Louis
COMMENT	MO 63108, USN
	On Mar16, 2001 this sequence version replaced gi:9211494.

JOURNAL MEDLINE REFERENCE AUTHORS TITLE	JOURNAL MEDLINE REFERENCE AUTHORS TITLE
1 (bases 1 to 1209)	1 (bases 1 to 1209)
Howard, A.D., Wang, R., Pong, S.S., Mellin, T.N., Strack, A., Guan, X.M., Zeng, Z., Williams, D.L., Jr., Peighner, S.D., Nunes, C.N., Murphy, B., Stair, J.N., Yu, H., Jiang, Q., Clements, M.K., Tan, C.P., McKee, K.K., Hrenkul, D.B., McDonald, T.P., Lynch, K.R., Evans, J.F., Austin, C.P., Caskey, C.T., Van der Ploeg, L.H. and Liu, Q.	Howard, A.D., Wang, R., Pong, S.S., Mellin, T.N., Strack, A., Guan, X.M., Zeng, Z., Williams, D.L., Jr., Peighner, S.D., Nunes, C.N., Murphy, B., Stair, J.N., Yu, H., Jiang, Q., Clements, M.K., Tan, C.P., McKee, K.K., Hrenkul, D.B., McDonald, T.P., Lynch, K.R., Evans, J.F., Austin, C.P., Caskey, C.T., Van der Ploeg, L.H. and Liu, Q.
Identification of receptors for neuromedin U and its role in feeding	Identification of receptors for neuromedin U and its role in feeding
Nature 406 (6791), 70-74 (2000)	Nature 406 (6791), 70-74 (2000)
2 (bases 1 to 1209)	2 (bases 1 to 1209)
Liu, Q., McDonald, T.P., Wang, R., Jiang, Q. and Howard, A.D.	Liu, Q., McDonald, T.P., Wang, R., Jiang, Q. and Howard, A.D.
Direct Submission	Direct Submission
Submitted (09-MAR-2000) Pharmacology, Merck Research Labs West	Submitted (09-MAR-2000) Pharmacology, Merck Research Labs West

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      /gene="NM01R"
CDS 1. .1209
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84 CTTGGGGCCACAGCAGGTAACAAATTTTGGCCCATCTGTGTACAGTACCTGTTGATCTT 143

159 tctgtgtgsggtcatttgcaatgtccctgtgtgcctgtgattctgcagcaccagctat 218

144 CGTAGTGGGCACTCTGGGCAACGGGTTGACCTGCACCGTCATCTCGGCCAGAACGCAAT 203

219 gaagagcgcacccaactactactactctctcagccttgccgtgcgctctcttaacclcctgaatcctact 278

204 GCACAGCCCCAACCTTCACTCTTCATGTCGGGTSTCCCAATTGCCCGCCTCCCTCC

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CCACCCAGGACCTTATGAGATGCAGCACATTACCCATTCCAGCTGGTGC 323

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Db	324	AGGTGGCTTTAACTTCCGAAATACTGCTTTTGGAGACTGTCCCTGGGTCAAGTGCAA	383
QY	399	catcaacacacgttcacgtctggagagcgtactgttgacatccctaacaccgtcttcgcgcgaact	458
Db	384	TTCTACAGCCCTAAGTGTGGAGCGTTATGTGGCCGTGGTGTGCACCCACTCCAAAGCAAGTC	443
QY	459	gcagagcaaccgcgcgcgcgggacctcaagatccttcgcgatcgtctcgggtctccgtgct	518
Db	444	TGTGATGACAGCGACCCCATGTGCGCCCGCATGTGTGGAGGCATCTGGGGTCTTCCGTATTCT	503
QY	519	cttctccctgtcccaaccaccgacatccatgcatcaagttccactacttcccacatggtc	578
Db	504	CTTCTCTGTGCCAAACACCACTTACATGGCTTCACATCCACTATGTACCTGCCGGGG	563
QY	579	ccgtgtccacaggttcgcgcacgtctaacgttcatcaagcccatgtgatatcaaatltcat	638
Db	564	GCCGGTGGCCGATTCAGTTAGTACGTACCGCTGGTGGCTGCCCAAGTCTTCTACAAAGTTGGT	623
QY	639	catccagtgatccctcctctcctatctactcctccaccatgaatcgtcatatgattctctca	698
Db	624	AATACAGACGACCATTAAGTCTCTCTCTCTGCTGTGCGCATGTACCATCATAGTGTCTGTA	683
QY	699	ctactcatgtgacactcagatgagatctcag	729
Db	684	CTTCTCATTTGGCTGTGAGCTGTGGAGGGAG	714

RESULT	12
LOCUS	AB038649
DEFINITION	AB038649 1239 bp mRNA
ACCESSION	Rattus norvegicus mRNA for G protein-coupled receptor FM-3, complete cds.
VERSION	AB038649
KEYWORDS	AB038649.1 GI:9049392
SOURCE	G protein-coupled receptor FM-3.
ORGANISM	Rattus norvegicus cDNA to mRNA.
	Rattus norvegicus

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE

1 (sites)
Fujii, R., Hosoya, M., Fukusumi, S., Kawamata, Y., Habata, Y., Hinuma, S., Onda, H., Nishimura, O., and Fujino M.
Identification of neuromedin u as the cognate ligand of the orphan G protein-coupled receptor FM-3
J. Biol. Chem. 275 (28), 21068-21074 (2000)
20347213

REFERENCE
2 (bases 1 to 1239)
Fukusumi, S., Fujii, R. and Hinuma, S.
Direct Submission
Submitted (22-FEB-2000) to the DDBJ/EMBL/Genbank databases, Shujie
Hinuma, Takeda Chemical Industries, Ltd., Discovery Research
Laboratories 1, Wada 10, Tsukuba, Ibaraki 300-4293, Japan
(Fax: 81-298-64-5000) Shujie@takeda.co.jp, Tel: 81-298-64-5035,
Fax: 81-298-64-5000)

FEATURES	Location/Qualifiers
source	1. .1239

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/organism=Rattus norvegicus
/db_xref="taxon:10116"

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          /gene="FM-3"
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CDS 1. .1239 /gene="FM-3"

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/product="G

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/product = 0
/protein_id=
/db_uni6=not

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/usr_x86_64-linux-gnu/translation
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KÖELPICVYLL
LELYEMQHNYPF

RESULT 14
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LOCUS AC073449 75950 bp DNA HTG 18-JUN-2000
DEFINITION Homo sapiens clone RP11-154A7, LOW-PASS SEQUENCE SAMPLING.
AC073449
AC073449.1 GI:8571740
VERSION HTG: HTGS-PHASED.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 75950)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens, clone RP11-154A7
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 75950)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavskiy, L., Boukhalter, B., Brown, A., Burkett, G., Campiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domingo, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Hearford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karakas, A., Klein, R., Lien, C., Liu, G., Locke, K., Landers, T., Lehotzky, J., Levine, R., Mewen, P., McGuirk, A., McDonald, P., Margulis, N., McCarthy, M., Menus, L., Mihova, T., Miranda, C., Mlenka, V., Morrow, J., Murphy, T., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisanic, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zahoun, J., Zimmer, A. and Zody, M.
DIRECT SUBMISSION
Submitted (18-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIPR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10390
Center clone name: 154_A_7

* NOTE: This record contains 92 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1
* 734 833: contig of 733 bp in length
* 834 1540: gap of 100 bp
* 1541 1640: contig of 707 bp in length
* 1641 2334: gap of 100 bp
* 2335 2434: contig of 694 bp in length
* 2435 3156: gap of 100 bp
* 3157 3256: contig of 722 bp in length
* 3257 3981: gap of 100 bp
* 3981: contig of 725 bp in length

3982 4081: gap of 100 bp
4082 4828: contig of 747 bp in length
4829 4928: gap of 100 bp
4929 5658: contig of 730 bp in length
5659 5758: gap of 100 bp
5759 6493: contig of 735 bp in length
6494 6593: gap of 100 bp
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7330 7429: gap of 100 bp
7430 8169: contig of 740 bp in length
8170 8269: gap of 100 bp
8270 8974: contig of 705 bp in length
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9807 9906: gap of 100 bp
9907 10636: contig of 730 bp in length
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10737 11426: contig of 690 bp in length
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11527 12261: contig of 735 bp in length
12262 12361: gap of 100 bp
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16472 16571: gap of 100 bp
16572 17304: contig of 733 bp in length
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17405 18113: contig of 709 bp in length
18114 18213: gap of 100 bp
18214 18940: contig of 727 bp in length
18941 19040: gap of 100 bp
19041 19753: contig of 713 bp in length
19754 19853: gap of 100 bp
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20652 21378: contig of 727 bp in length
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21479 22207: contig of 729 bp in length
22208 22307: gap of 100 bp
22308 23029: contig of 722 bp in length
23030 23129: gap of 100 bp
23130 23872: contig of 743 bp in length
23873 23972: gap of 100 bp
23973 24699: contig of 727 bp in length
24700 24799: gap of 100 bp
24800 25534: contig of 735 bp in length
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25635 26371: contig of 737 bp in length
26372 26471: gap of 100 bp
26472 27211: contig of 740 bp in length
27212 27311: gap of 100 bp
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Query Match	18.5%;	Score 134.8;	DB 88;	Length 2040;
Best Local Similarity	56.1%;	Pred. No. 2.6e-16;		
Matches 275;	Conservative 0;	Mismatches 212;	Indels 3;	Gaps 1

Query Match	18.5%	Score 134.8	DB 88	Length 2040
Best Local Similarity	56.1%	Pred. NO. 2.6e-16		
Matches 275	Conservative	0	Mismatches 212	Indels 3
			Gaps	
QY	128	tcoccgatgctgtgtgtatgtgccaatlttgttggvvggtcaattgtgcattgtcctgg	187	
Db	116	tcgcctgtaccccttctgttgcctgttcctgttgcctgttgcctgtgcgggtgacggcaacgngga	176	
QY	188	tgltgcgtgtatcttcgcagcacccagctatgaagaagccaccactactacttca	24	
Db	176	ccgtgatgtgattcgggggctacggggacatnccggaccaccacacacttgtacctggaca	235	
QY	248	gctctggcgctcttgaacctcttgttctgtcttcttcttgaagtgcccttgaagttcataga	307	
Db	236	gcattggccgtgtccacacttacttacttgcctc---ggcgctccgcttgaccttgaccgcc	292	
Y	308	tgtggcgaactaaccttcttgttgcggcccggtgggtgttacttcaagaagccctc	367	
Db	293	tctggcgcgtcggggccctgggggttccggccgctgttgcctgttcccttgccttgacgtgg	352	
QY	368	ttgagacggtgtgtcttgccttcacatcctcagcatcacacccgtacagcttgaagcgtacg	427	
Db	333	gcgaaggctgcacacttaccacccacgtgtgcacatgaccgcggccttcaggctgagagcgttacc	412	
QY	428	tggccatctaacaccgcttccgcgcgaacatcgcaagcagcccgcgcccgccctcaaga	487	
Db	413	tggccatcttgccggccgcttccggcccccgcgttggcttgcacccggccgcttccggccgc	472	
QY	488	tctctgcgcatcgttctggggcttctcgttgtctcttcccttgcgaacacagcatcatg	547	
Db	473	tcatctgcgtctctggggcccttgccgctgcttctgcggcttcccttcttcttcttcttcttctt	532	
QY	548	gcataagttccaatcttcccaatbfgccctgtgcccaggttgcgcactgtacag	607	
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QY	608	tcatcaagcc	617	
Db	593	cttctctgcgc	602	

Search completed: August 30, 2001, 02:49:04
Job time: 20471 sec

Genomic sequence of
DNA encoding the p
Human neurotensin
cDNA encoding canli
Human growth hormo
Human growth hormo
Human G protein-co
DNA encoding human
Human G protein-co
Human growth hormo
Human growth hormo
Pig growth hormone
Swine growth hormone
Pig growth hormone
Swine growth hormo
DNA encoding the m
Human D4 receptor
Recombinant human
Allele DA.2 of the
Recombinant human
Allele DA.7 of the
cDNA encoding the
Allele DA.4 of the
Rat growth hormone
Rat growth hormone
Rat growth hormone
Rat THR receptor 2
Human NT2LP1 protein
cDNA encoding a hu
Human NT2LP1 protein
Galatin receptor G
Galatin receptor G
Galatin receptor G

PR	28-MAY-1999;	9905-01364.3
PR	28-MAY-1999;	9905-01365.67
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PR	28-JUN-1999;	9905-01414.48
PR	28-SEP-1999;	9905-01565.55
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PR	28-SEP-1999;	9905-01566.34
PR	28-SEP-1999;	9905-01566.53
PR	01-OCT-1999;	9905-01567.83
PR	01-OCT-1999;	9905-01572.81
PR	01-OCT-1999;	9905-01572.82
PR	01-OCT-1999;	9905-01572.93
PR	01-OCT-1999;	9905-01572.94
PR	12-OCT-1999;	9905-04167.60
PR	12-OCT-1999;	9905-04170.44

Claim 21; Page 56-57; 102pp; English.

The present sequence is a cDNA encoding hrup6, an endogenous human orphan G protein-coupled receptor (GPCR). The full length hrup6 cDNA was cloned by RT-PCR using human thymus cDNA as template. The orphan GPCR of the invention, like all GPCRs has seven transmembrane α helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins may also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states.

Sequence 1248 BP; 269 A; 393 C; 269 G; 317 T; 0 other;

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Best Local Similarity	99.7%;	Pred. No. 3.3e-146;		
Matches 719; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY	1	atggaanaacttcagaaatgccttccttcgtatctacagaagaanaactcagaagaatccattccag	60
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QY	61	aaacacctgacacagcaacgagagatccttccttccttcgcgagactcgcgcagaccac	120
Db	70	aaacacactgacacagcaacgagagatccttccttccttcgcgagactcgcgcagaccac	129
QY	121	tcttcctcccgctgctctgctgctgctatcgtccaaattttctgtgtgaggtcatttggcaat	180
Db	130	tcttcctcccgctgctctgctgctgctatcgtccaaattttctgtgtgaggtcatttggcaat	189
QY	181	gtccctgctgctcctgctgctatcttcctgcagcaacagactatgaagagcccccacaaactaac	240
Db	190	gtccctgctgctcctgctgctatcttcctgcagcaacagactatgaagagcccccacaaactaac	249
QY	241	cctcttaacgtcgcgctctctcctgaacctcctgctccttccttcgtgaatgccctctgaagtc	300
Db	250	cctcttaacgtcgcgctctctcctgaacctccttccttccttcgtgaatgccctctgaagtc	309
QY	301	tatgagatgctgctgacacaaacctctctcttccttcggagcccgctggctgctactccaagacg	360
Db	310	tatgagatgctgctgacacaaacctctctcttccttcggagcccgctggctgctactccaagacg	369

Db	310	tatgagatgttgcgcaactaaccttctctgttcggtgcccgtgtctaattcaagacg	369
Qy	361	gacctctttgaagaccgtttgtcttgccctcaatctctcaagatcaaccacgttcagcttgag	420
Db	370	gacctctttgaagaccgtttgtcttgccctcaatctctcaagatcaaccacgttcagcttgag	429
Qy	421	cgcctacgtggccatcctctacaccggtttccgcgcaaatgcagagacaccggtcgccgagcc	480
Db	430	cgcctacgtggccatcctctacaccggtttccgcgcaaatgcagagacaccggtcgccgagcc	489
Qy	481	ctcagatctccgcgcatctgctcttggggtctctcgttgctcttctccttcgcgaacacagc	540
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Qy	541	atccatgtgcataaatttccattacttccccaatgagtggtccctgtgtccaggttgcgcacc	600
Db	550	atccatgtgcataaatttccattacttccccaatgagtggtccctgtgtccaggttgcgcacc	609
Qy	601	tgtacggtcatcaagcccacatgttgatctacaaattcatcatcaggtacactctctcta	660
Db	610	tgtacggtcatcaagcccacatgttgatctacaaattcatcatcaggtacactctctctta	669
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Db	730	a 730	
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AC	AAAA6022;		
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DT	22-AUG-2000 (first entry)		
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DE	Human G protein coupled receptor hrup6 encoding cDNA SEQ ID NO:11.		
XX			
KW	Human; G protein coupled receptor; GPCR; transmembrane receptor;		
KW	identification; agonist; screening; therapeutic; pharmaceutical;		
XX	mutant; SS.		
XX			
OS	Homo sapiens.		
XX			
FN	WO200022131-A2.		
XX			
PD	20-APR-2000.		
XX			
FE	13-OCT-1999;	99WO-US24065.	
XX			
XX	13-OCT-1998;	98US-0170496.	
XX	12-NOV-1998;	98US-0108029.	
PR	20-NOV-1998;	98US-0109213.	
PR	27-NOV-1998;	98US-0110060.	
PR	16-FEB-1999;	99US-0120416.	
PR	26-FEB-1999;	99US-0121852.	
PR	12-MAR-1999;	99US-0123944.	
PR	12-MAR-1999;	99US-0123945.	
PR	12-MAR-1999;	99US-0123946.	
PR	12-MAR-1999;	99US-0123948.	
PR	12-MAR-1999;	99US-0123949.	
PR	12-MAR-1999;	99US-0123951.	
PR	28-MAY-1999;	99US-0136436.	
PR	28-MAY-1999;	99US-0136437.	
PR	28-MAY-1999;	99US-0136439.	
PR	28-MAY-1999;	99US-0137127.	
PR	28-MAY-1999;	99US-0137131.	
PR	28-MAY-1999;	99US-0137567.	
PR	30-JUN-1999;	99US-0141448.	
PR	27-AUG-1999;	99US-0151114.	

PR 03-SEP-1999; 99US-0152524.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156634.
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Behan DP, Lehmann-Brinsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
 DR WPI: 2000-317986/27.
 DR P-PSDB: AAB02830.
 XX
 PT Non-endogenous, human G protein-coupled receptors for screening
 PT receptor, inverse or partial agonists useful as therapeutic agents -
 XX
 XX
 XX Example 1; Page 85-86; 187pp: English.
 CC
 CC The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCR), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for
 CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAAAA6017 to AAAAA6126 and AAB02825 to AAB02859 represent sequences used in
 CC the exemplification of the present invention.
 XX
 XX Sequence 1248 BP; 269 A; 393 C; 269 G; 317 T; 0 other;

Query Match	Similarity	98.5%	Score	717.8	DB	21	Length	1248
Best Local	Similarity	99.7%	Pred.	No.	3.3e-146			
Matches	719	Conservative	0	Mismatches	2	Indels	0	Gaps
QY	1	atggaanaaactcagaatgctctccgagatctacaccagaaactagaaatccattccag	60					
Db	10	atggaanaaactcagaatgctctccgagatctacaccagaaactagaaatccattccag	69					
QY	61	aaaccccggaacagacacccgagagatcttgctctccctctgtgagaccttggcagagccac	120					
Db	70	aaaccccggaacagacacccgagagatcttgctctccctctgtgagaccttggcagagccac	129					
QY	121	tctctccctcccggtgtcctgtggtatgtagtgacaaattttgtgtgtgtgtgtgtgtgtgtgt	180					
Db	130	tctctccctcccggtgtcctgtggt	189					
QY	181	gtccctggt	240					
Db	190	gtccctggt	249					
QY	241	ctcttcacagcttgcggtgtctctgcacctctgtctctgtctctgtctctgtctctgtctctgt	300					
Db	250	ctcttcacagcttgcggtgtctctgcacctctgtctctgtctctgtctctgtctctgtctctgt	309					
QY	301	tatgagatgt	360					
Db	310	tatgagatgt	369					
QY	361	gcccctcttgagacccgt	420					
Db	370	gcccctcttgagacccgt	429					
QY	421	cgcctacgt	480					
Db	430	cgcctacgt	489					
QY	481	ctcagagatcccttcgagatgtctgt	540					
Db	490	ctcagagatcccttcgagatgtctgt	549					
QY	541	atccatgtgcatcaagttcccaacttcccacaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	600					

Db	550	atccatggaacaaagtctccatacttccccaatgggtccctggtcccaagttcggccacc	609
QY	601	tgtacgcatcatcaagacccaatgttgatctctacaatttcatacatccaggtccactccctcta	650
Db	610	tgtacgcatcatcaagcccatgttgatctctacaatttcatacatccaggtccactccctcta	659
QY	661	tcttaaccctcccccacatgacatgtcataagtgctctctactactccctcaatgggaactccagaatg	720
Db	670	tcttaaccctcccccacatgacatgtcataagtgctctctactactccctcaatgggaactccagaatg	729
QY	721	a 721	
Db	730	a 730	

RESULT	3
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ID	AAZ33297 standard; CDNA; 1360 BP.
XX	
AC	AAZ33297;
XX	
DT	21-FEB-2000 (first entry)
XX	
DE	Human neurotensin-like receptor encoding cDNA.
XX	
KM	Human; neurotensin-like receptor; NLR: G-protein coupled receptor;
KM	central nervous system; anesthesia; analgesia; ds.
OS	Homo sapiens.
XX	
PN	W0955732-A1.
XX	
PD	04-NOV-1999.
XX	
PF	15-APR-1999; 99WO-SE00598.
PR	24-APR-1998; 98SE-0001455.
XX	
PA	(ASTR-) ASTRA PHARMA INC.
PA	(ASTR) ASTRA AB.
XX	
PI	Ahmad S, Cao J, O'Donnell D, Walker P;
XX	
DR	WPI; 2000-052803/04.
XX	
DR	P-PSDB; AAY52992.
PT	Novel neurotensin-like receptor, useful for identifying agents for
PT	producing anaesthesia or analgesia -
XX	
ES	Claim 11; Fig 1; 46pp; English.
XX	
CC	The present sequence encodes a human G-protein coupled receptor
CC	neurotensin-like receptor (NLR). The NLR polynucleotide and protein
CC	can be used to isolate compounds that bind, (antagonise or alter
CC	the activity or expression of the NLR. The NLR is a G-protein coupled
CC	receptor which is expressed in the central nervous system and shares in
CC	homology with human neurotensin receptor. The receptors can be used in
CC	assays to identify agents for producing anaesthesia and analgesia.
XX	
SQ	Sequence 1360 BP; 293 A; 423 C; 294 G; 350 T; 0 other;
Query Match	98.5%; Score 717.8; DB 21; Length 1360;
Best Local Similarity	99.7%; Pred. No. 3.3e-146;
Matches 719; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY	1 atgggaanaacttcagaatagctcctcgatactacccagcaagaactagaaatccattccag 60
Db	74 atggaanaaacttcagatagctcttcgagtctaccagcagaactagaaatccattccag 133
OY	61 aaacacctgaaacagaccgcaggagatatcttgacctctctcgtgcgacccgcgcagccac 120
Db	134 aaaacccctgaaacagaccgcaggagatatcttgacctctctcgtgcgacccgcgcagccac 193

us-09-684-725-1.rng

ID	AAF76231 standard; cDNA; 1209 bp.
XX	AAF76231;
NC	
XX	
DW	
DE	05-JUN-2001 (first entry)
XX	
XX	Human G-protein coupled receptor
KW	Human; FM-3; G-protein coupled receptor FM-3 cDNA.
KW	Ligand screening; agonist identification; function determination;
KM	signal transduction disorder; drug discovery; drug design; ss.
XX	
OS	Homo sapiens.
PN	WO200114863-A1.
PN	
XX	
PD	01-MAR-2001.
XX	
XX	
XX	23-AUG-2000; 2000MO-JP05639.
PR	
XX	24-AUG-1999; 99JP-0236557.
PA	(TAKE) TAKEDA CHEM IND LTD.
XX	
PI	Hinuma S, Hosoya M,

[illegible]

RESULT 5
AAA30663 standard; cDNA; 1212 BP.
ID AAA30663 standard; cDNA; 1212 BP.
XX
XX
XX
XX
XX
21-AUG-2000 (first entry)
XX
XX
DE Human G protein-coupled receptor MIG cDNA.
G protein-coupled receptor; GPCR; constitutively active;
intracellular loop 3; transmembrane domain 6; drug screening;
agonist; antagonist; ss.
XX
XX
OS Homo. sapiens.
PN MO200022129-A1.
PD 20-APR-2000.
XX
XX
XX 12-OCT-1999; 99MO-US23938.
XX
XX 13-OCT-1998; 98US-0170496.
PA (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Chalmers DT, Liaw CW;
XX WPI: 2000-329165/28.
DR P-PSDB; AAY90638.
XX
XX
XX Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents -
XX
XX
XX Example 1; Page 188-189; 341pp; English.
XX
XX
XX The invention relates to constitutively active, non-endogenous versions
XX of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
XX AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
XX and AAA30775-A30779). The mutant proteins of the invention contain a
XX mutation in a portion of the protein comprising intracellular loop 3
XX (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
XX is substituted for an endogenous residue in IC3 at a position 16 amino
XX acids N-terminal of an endogenous proline in TM6 to form a sequence
XX X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
XX or Ala, and is preferably Lys. When the endogenous residue at this
XX position is Lys, this residue is replaced by His, Arg or preferably Ala.
XX The 15 amino acid stretch between the substituted amino acid and the Pro
XX may be endogenous, non-endogenous, or a mixture of endogenous and
XX non-endogenous residues. The constitutively active GPCRs are useful for
XX identifying antagonists, agonists and partial agonists for use as
XX pharmaceutical agents. The mutant proteins are also useful in research
XX settings for elucidating the roles of the receptors in normal and
XX diseased conditions. Antagonists for a particular GPCR are useful for
XX treating diseases and disorders associated with that receptor. Because
XX the novel mutant GPCRs are constitutively active, they can be used
XX directly for screening of compounds without the need for endogenous

OY	103	ggacctgvgcgagcacccttcttcctcccglygtcgtgntgtatgtagtgccaatttttg	162
Db	88	gggcaccccgagcaagaagctgtlcatbgcccactcgtgcacaataccgcgtgatcttctg	147
OY	163	gtggaggctatgtgcgaagtccctgltgagcttgtgtatcttcgcagacccaggatgaag	222
Db	148	gtggcgctgtgvggcaaatgggcttgaccctgcttctgtcatctctgcgcacaaggccaatgcgc	207
OY	223	acgcaccaaacatactactcctctcaagccttgccgylctcttgacacccctcgttctcct	282
Db	208	acgctaccaaactactactcctcttcaagccttgccgyltgagacctgtgltgctgtcgtg	267
OY	283	ggaaatgccctcgagaggtctatagatatgtgvcgcacaatacccttcttgttcggccctg	342
Db	268	ggccctgccttggagctctatagaaatgtgycacaataccccctctcgtcgtgagcttgyt	327
OY	343	ggctcctaactcaagaagcgcctctctttagagccgtgtgcttgccctgcatacctcaagtc	402
Db	328	ggctgctatcttcgcagcgtactcgttttgagatgtgtctgcctgcgtccatagtgtccaagctc	387
OY	403	accacccgctcaagctgttgagagcgttaagtggtgcatacccttatccgcgcgccaacttgag	462
Db	388	actgcctcgagcgtgtggaagcgtatgtggtccgtgtgttgaccccaatccagggccaagtccatg	447
OY	463	agcacccggcgccgggcccctcaagatccctcgtgcatacgtcttggtggtctctccgtgtcttc	522
Db	448	gtgaagcggcgcccaatgtgcgcggagtgcttbtgggcgcgtcttggtgtcttgacgtctctgc	507
OY	523	tccctggcccaacacagagatccatagagcataagttccaactctccccaatlggttccctg	582
Db	508	tccctggcccaaacacagcgtgcacggcatccggcgaagctgcgcgtgacctgtccggggccca	567
OY	583	gtcccaagtltcggccaacctgtgacggtcaatacgaagccocatgtgatatctacaatlcatcatc	642
Db	568	gtgcgaagcgtcaagctgtttgtcatgtctgtgtccgcacagggccctctacaacatgtgtagtg	627
OY	643	cagtgtaacctcttcctcatcttbaacctcctcccaatgagctgcatcaagtgtcctctactac	702
Db	628	cagacacacacgcgtctctctctctctctctctcgtcccatgscatcatgagcgtgctctactctg	687
OY	703	ctcatgtgcactcagaagttag	722
Db	688	ctcatgtggtcgtgcagctcg	707
RESULT 6			
AAA30739			
ID	AAA30739 standard; DNA; 1212 BP.		
XX			
AC	AAA30739;		
XX			
DT	21-AUG-2000 (first entry)		
XX			
DE	DNA encoding human mutant G protein-in-coupled receptor MIG (T273K).		
XX			
KW	G protein-coupled receptor; GPCR; constitutively active;		
KM	intracellular loop 3; transmembrane domain 6; drug screening;		
KW	agonist; antagonist; mutant; ss.		
XX			
OS	Homo sapiens.		
05	Synthetic.		

QY 403 accacgcgtcaagcgtgagcgctactggtgcatccctacaccggttcgcgcgaactgcag 462
 Db 696 acagccctgagtggtgagcgcttattgtgcccgtgtgtgcccacacgaagctcgtg 755
 QY 463 agacccggcgccggcgccccaagatctctgcgtcgtctgcgggtcttcgtctcttc 522
 Db 756 atgacaaggcgccatgtgcgcgcgcatgtggtgggcatctgggtcttcgtactcttc 815
 QY 523 tccctgccaacacacgaatcatatgcatcaagttccactctccccaatggtccctg 582
 Db 816 tctctgccaacacacgaatcgtatgcatcaagttccactctccccaatggtccctg 875
 QY 583 gtcccggttcgcgcacactgtatgcatcaagccatgtgtgatacaattcaccatc 642
 Db 876 gtgcgcgcacacgcatatgtgtcgtgtgtgtgcacatgacttcaagtgtgtgta 935
 QY 643 caagtcacccctctctatctacccctccccaatgcatcgtatcgtctctctacac 702
 Db 936 ctgactacgcgactgtctctctctctctctgctcccatgtcatcactggtgtatctg 995
 Y 703 ctcatgtgacactgagatgtgatctag 729
 Db 996 ctcatgtggtcgtgcgtgcgagggag 1022

RESULT 9

AAZ45403

ID AAZ45403

standard; cDNA; 1239 BP.

AAZ45403;

27-MAR-2000 (first entry)

cDNA encoding the motilin receptor splice variant MTL-R1A.

MTL-R1A receptor; G-protein coupled receptor; MTL-R1; GPR38;
 spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;
 functional defect; neurological disorder; scleroderma; colonoscopy;
 paraneoplastic syndrome; radiation induced dysmotility; diabetes;
 infection; stress-related motility disorder; psychogenic disorders;
 gastroparesis; gastro-oesophageal reflux disease; constipation;
 chronic idiopathic pseudo obstruction; acute faecal impaction;
 postoperative ileus; gallstones; infantile colic; diarrhoea;
 irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;
 endoscopy; duodenal intubation; ds.

Homo sapiens.

Key Location/Qualifiers
 1..1239
 /*tag= a
 /product= "MTL-R1A"

W09964436-A1.

16-DEC-1999.

08-JUN-1999; 99W0-U0512773.

12-JUN-1998; 98US-0089098.

(MERI) MERCK & CO INC.

Feighner SD, Patchett AA, Tan C, McKee K, MacNeill D, Howard AD;
 Pong S, Smith RG;

WPI: 2000-105868/09.

P-PSDB; AA154145.

Novel receptor protein for screening compounds used in treating
 irritable bowel syndrome, constipation and other gastric conditions

PS Claim 4: Fig 2: 44pp: English.

XX The present sequence encodes splice variant MTL-R1A of the motilin
 CC receptor. The gene encodes a G-protein coupled receptor, and is
 CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist,
 CC MTL-R1A (see AA154145) and MTL-R1B (see AA154146). MTL-R1A is a
 CC functional seven transmembrane domain form, and MTL-R1B is a truncated
 CC five transmembrane domain. The MTL-R1 proteins are used to identify
 CC agonists and antagonists which can be used for treating gastric motility
 CC disorders, functional defects, disorders secondary to neurological
 CC disorders e.g. scleroderma, paraneoplastic syndromes radiation induced
 CC dysmotility, diabetes, infections, stress-related motility disorders,
 CC psychogenic disorders, gastroparesis, gastro-oesophageal reflux disease,
 CC constipation, chronic idiopathic pseudo obstruction, acute faecal
 CC impaction, postoperative ileus, gallstones, infantile colic, irritable
 CC bowel syndrome, non-ulcer dyspepsia, non-cardiac chest pain and
 CC diarrhoea. They can also be used in the preparation for colonoscopy,
 CC endoscopy and duodenal intubation.
 SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 other;

Query Match 18.5%; Score 134.8; DB 21; Length 1239;
 Best Local Similarity 56.1%; Pred. No. 2e-20;
 Matches 275; Conservative 0; Mismatches 212; Indels 3; Gaps 1;

QY 128 tcccgctgctgtgtgtatgtgccaaatttctgtgtggtgggtcattgcaatgtcctg 187
 Db 116 tgcggtgacccgctgtgtgtcctgtgtcgtgtcgtgtgtgtgtgtgtgtgtgtgt 175
 QY 188 tgtcgtgtgtatctgcagacacgcatatgaagacgcccacacactactactctca 247
 Db 176 ccgtgattgctgattcgtgcgtcaccggtacatgcggaccacacactgtactctgga 235
 QY 248 gctcgtggtctctgacctcctcgtcctgtcctctgtgaatgcctgtgaggtctataga 307
 Db 236 gcatggtcgtgtcgcacactactactcctgtctc---gggtcgtcgtcgtcgtcgtcgtc 292
 QY 308 tgtgccaactacacccctctctgtgtgtggtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 367
 Db 293 tctggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 352
 QY 368 ttgagcgtgtgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 427
 Db 353 gcgaggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 412
 QY 428 tggcattcctacacccgttctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 487
 Db 413 tggcattcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 472
 QY 488 tctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 547
 Db 473 tcatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 532
 QY 548 gcatcaagtccactcctcccaatggtccctgtgtcccaatggtcgtcgtcgtcgtcgtcgtc 607
 Db 533 gcgtc 607
 QY 608 tcatcaagcc 617
 Db 593 cctcctcgtcgc 602

RESULT 10

AAZ45404

ID AAZ45404

standard; cDNA; 1390 BP.

AAZ45404;

27-MAR-2000 (first entry)

cDNA encoding the motilin receptor splice variant MTL-R1B.

Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;
 KW spliced form: MTL-RIA; MTL-RIB; gastric motility disorder;
 KW functional defect; neurological disorder; scleroderma; colonoscopy;
 KW paraneoplastic syndrome; radiation induced dysmotility; diabetes;
 KW infection; stress-related motility disorder; psychogenic disorder;
 KW gastroparesis; gastro-esophageal reflux disease; constipation;
 KW chronic idiopathic pseudo obstruction; acute fecal impaction;
 KW postoperative ileus; gallstones; infantile colic; diarrhoea;
 KW irritable bowel syndrome; non-ulcer dyspepsion; non-cardiac chest pain;
 KW endoscopy; duodenal intubation; ds.
 XX
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..1161
 FT /tag=a
 FT /product= "MTL-RIB"
 XX
 PN MO9964436-AI.
 XX
 PD 16-DEC-1999.
 XX
 PF 08-JUN-1999; 99MO-US12773.
 XX
 PR 12-JUN-1998; 98US-0089098.
 XX
 PA (MERI) MERCK & CO INC.
 PI Feighner SD, Patchett AA, Tan C, McKee K, MacNeil D, Howard AD,
 PI Pong S, Smith RG;
 DR WPI: 2000-105868/09.
 XX
 DR P-PADB; AAY54146.
 XX
 PT Novel receptor protein for screening compounds used in treating
 PT Irritable bowel syndrome, constipation and other gastric conditions -
 XX
 XX Claim 6; Fig 4; 44pp; English.

The present sequence encodes splice variant MTL-RIB of the motilin
 CC receptor. The gene encodes a G-protein coupled receptor, and its
 CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist,
 CC MTL-RIA (see AAY54145) and MTL-RIB (see AAY54146). MTL-RIA is a
 CC functional seven transmembrane domain form, and MTL-RIB is a truncated
 CC five transmembrane domain. The MTL-R1 proteins are used to identify
 CC agonists and antagonists which can be used for treating gastric motility
 CC disorders, functional defects, disorders secondary to neurological
 CC disorders e.g. scleroderma, paraneoplastic syndromes radiation induced
 CC dysmotility, diabetes, infections, stress-related motility disorders,
 CC psychogenic disorders, gastroparesis, gastro-esophageal reflux disease,
 CC constipation, chronic idiopathic pseudo obstruction, acute faecal
 CC impaction, postoperative ileus, gallstones, infantile colic, irritable
 CC bowel syndrome, non-ulcer dyspepsion, non-cardiac chest pain and
 CC diarrhoea. They can also be used in the preparation for colonoscopy,
 CC endoscopy and duodenal intubation.
 XX

Sequence 1390 BP; 190 A; 496 C; 436 G; 268 T; 0 other;

Query Match 18.5%; Score 134.8; DB 21; Length 1390;
 Best Local Similarity 56.1%; Pred. No. 2.le-20;
 Matches 275; Conservative 0; Mismatches 212; Indels 3; Gaps 1

DQ 128 tccctgtgcttggatgtcgaacatttggtggtgggcattggcaactgctcg 187
 ||||| ||||| || | ||||||| ||||| |||||
 DB 116 tcgcggtaaccgcttgttcctgtgacctttcgtgctgggltgagcgacaagtgtga 175
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 188 tgctcgtgatctctcgcagcacccaggcatagaagacgccccaactacactcca 247
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 176 ccgtgatgctgatacggcgctacacggagacatcgagacaccaaacattgtactatggaca 235
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 248 gctctgacggtctctctgctcgtgctctgctctctggaatgcccccctggaggtctatgaga 307
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

D6	226	gcattgcccgtatgccgaacttaacttcctgctc---ggcgctccggttgcacctgtaacgcc	292
OY	308	tctgagcaactaacctctcttgcttgaggccggtggagtctacttaagaacggccctc	367
D6	293	tctgagctctcgccgcctcggtttcttcgggccccgtctctctgcgcgtcttccctctaacgttg	352
OY	368	ctgaaaccgttgtcttgccctccaactcctaagcatcacacagctcagcgttagagcgttacg	427
D6	333	gcgaaggctctgacactcaacgcccacgctgtctgcaatgagaccgcgtcagaagctcagcgtaccc	412
OY	428	tggccatctcaacacccgtcttccgcccacaactctgacgaagacacccgagccgagccctcaga	487
D6	413	tggccatctgcccgcgcgcgtctccgagcccggtctgttgctcaaccgcgagcgcgtccgcgcgc	472
OY	488	tctctgagcatcgtctcbggggtctctccgttgctctctctcccttgcccacaacagatccata	547
D6	473	tcatcgtcgttgctcttgaggccgttgagcgtctgtctctctgcgcgtccctcttgttccgttg	532
OY	548	gcataagttcttcactactctccccaatggtgctcctgtgtlcccaagttcggaccaactgtlacg	607
D6	533	gcgtgaacgaggaaccccgacatctccgttgatgtccggagcctcaatgagcaccgcgagatcg	592
OY	608	tcatcaagcc 617	
D6	593	cctctctgcgc 602	
 RESULT 11 AAAA6116 ID AAAA6116 standard; cDNA; 2040 BP.			
AC	XX	AAAA6116;	
DT	XX		
DE	22-AUG-2000	(first entry)	
XX			
KM	Human G protein coupled receptor hGPR38 (V297K) cDNA SEQ ID NO:129.		
KW	Human; G protein coupled receptor; GPCR; transmembrane receptor;		
KM	Identification; agonist; screening; therapeutic; pharmaceutical;		
KW	mutant; ss.		
OS	Homo sapiens.		
OS	Synthetic.		
PN	WO200022131-A2.		
PD	20-APR-2000.		
PF	13-OCT-1999;	99WO-US24065.	
XX			
PR	13-OCT-1998;	98US-0170496.	
PR	12-NOV-1998;	98US-0108029.	
PR	20-NOV-1998;	98US-0109213.	
PR	27-NOV-1998;	98US-0110060.	
PR	16-FEB-1999;	99US-0120416.	
PR	26-FEB-1999;	99US-0121852.	
PR	12-MAR-1999;	99US-0123944.	
PR	12-MAR-1999;	99US-0123945.	
PR	12-MAR-1999;	99US-0123946.	
PR	12-MAR-1999;	99US-0123948.	
PR	12-MAR-1999;	99US-0123949.	
PR	12-MAR-1999;	99US-0123951.	
PR	28-MAY-1999;	99US-0136436.	
PR	28-MAY-1999;	99US-0136437.	
PR	28-MAY-1999;	99US-0136439.	
PR	28-MAY-1999;	99US-0137127.	
PR	28-MAY-1999;	99US-0137131.	
PR	28-MAY-1999;	99US-0137567.	
PR	30-JUN-1999;	99US-0141448.	
PR	27-AUG-1999;	99US-0151114.	
PR	03-SEP-1999;	99US-0152524.	
PR	29-SEP-1999;	99US-0156633.	
PR	29-SEP-1999;	99US-0156555.	

Db 480 ggcctctggtgcttgcgcctggtgctgcccgcctccacgcctcttcttctggtcgggtgga 539
 QY 555 gtccactacttcccccaatggtctccgtgtccacaggttcggcaacctgacgtcatcaa 614
 Db 540 gtacgaaacagagcagcaccgcactcaacacgggcacatgcagacacggctacgc 599
 QY 615 gccatgtgatctacaattcatcaccaggtaccctctctcatcttactcctcc 674
 Db 600 catcagctcgggagcagtcgacatcatgaltcgtgtgtccacccactcttcttgcgc 659
 QY 675 catgactgtatcagtgctcttacttactccatcagcactcagactagagtga 724
 Db 660 gatgctgtgtctccctcttctcctcaagctccatcgcgtggtgcaagctgtgga 709

RESULT 14

AAT33127
 ID AAT33127 standard; cDNA; 1254 BP.
 AC AAT33127;

07-NOV-1996 (first entry)

Human neurotensin receptor encoding sequence.

neurotensin receptor; antagonist; agonist; screening; treatment; ulcer;
 Parkinson's disease; depression; dementia; retrograde oesophagitis; ds.

Homo sapiens.

JP08143597-A.

04-JUN-1996.

24-NOV-1994; 94JP-0289882.

24-NOV-1994; 94JP-0289882.

(TAKE) TAKEDA CHEM IND LTD.

WPI; 1996-318958/32.

P-PSDB; AAR98562.

DNA encoding human neurotensin receptor protein - useful for
 screening for (ant)agonists used to treat, e.g. Parkinson's disease,
 depression, dementia, retrograde oesophagitis, ulcers, etc.

Claim 4; Page 22; 26pp; Japanese.

The present sequence encodes a human neurotensin receptor protein
 (AAR98562). The DNA and protein are useful for screening for
 (ant)agonists used to treat Parkinson's disease, depression, dementia,
 retrograde oesophagitis, ulcers, etc..

Sequence 1254 BP; 215 A; 459 C; 359 G; 221 T; 0 other:

Query Match 17.4%; Score 127; DB 17; Length 1254;
 Best Local Similarity 53.9%; Pred. No. 9, 9e-19;

Matches 337; Conservative 0; Mismatches 270; Indels 18; Gaps 3;

QY 114 cagccactcttccctcccgctgtctgtatgtgtaattttgtgtggggatcat 173
 Db 177 catctactcagaagtgtgtgacgcgctgtacctgctgtctgtgtggcacggt 236
 QY 174 tggcaatgtcctgtgtgtgtgtatcttcagcacccagcgctatgaagc----- 226
 Db 237 gggcaacacggtgacgggttcaacgctggcggaagaagtcgcagacgcttcagag 296
 QY 227 --ccacaactactactcctcagctggcggtctctgacccctcgtctcgtcttg 284
 Db 297 cacggtgacattacacacttgagcagcctggcgtgtctcagacctcgtctcgtgc 356

QY 285 aatgcccttgaggtcatgag--atgtggcgaactacccttcttctgttcgggccgt 341
 Db 357 catgcccgtggaagctgtacacttcatctgtgtgcaaccaccccttggccttcggcagc 416
 QY 342 gggcttactactaagaagccctctttgagaccgtgtgtctgcctccatcctcagcat 401
 Db 417 cggctgcgcgtactacttctctcgcgagccttgactacgtacgacgacctcaagct 476
 QY 402 caccacgcctgaggtgtgagcgtcagctgtgcacatccatcaccgcttcgcggcaactga 461
 Db 477 ggcacgcctgaggtgtgagcgtcagctgtgcacatccatcaccgcttcgcggcaact 536
 QY 462 gacacccggcgcggccctcagatccctcgcgcacatcgtctgggtcttcgtctt 521
 Db 537 catgtccgaagcgcgcacccaagaagttcatcagcgcacatctgtcgtcgtgcctgt 596
 QY 522 ctccctgcccacaacacagatcatcagatcgaatcactacttcccgaatggctcct 581
 Db 597 ggcgtgtcctatgtgttcaacatggcgagcagacgcagcgcgacg-----cca 650
 QY 582 ggtccaggttcggcacctgtacgtatcacaagccatgtgattatcaattatcat 641
 Db 651 gcaagccggcgccgtgtgtgcaaccccaacatccacactgcacccgtaaggtcgtcat 710
 QY 642 ccaggtaccctctctacttctactcctcccatgactgcatcaggtcctacta 701
 Db 711 acaggtcaacacttcatctcctcatatcccatgtgtgtcatctcgtctcgaac 770
 QY 702 cctcatgcactcaggtgagatc 726
 Db 771 catcatcgcacaacagctgacgctc 795

RESULT 15

AAZ61492
 ID AAZ61492 standard; cDNA; 1050 BP.

AAZ61492;

19-JUN-2000 (first entry)

CDNA encoding canine growth hormone secretagogue receptor (GHSR).

Canine; growth hormone secretagogue receptor; GHSR; dog; ss.

Canis sp.

Key Location/Qualifiers

FT CDS 1..1050 /tag= a /product= "growth hormone secretagogue receptor"

WO200009538-A2.

24-FEB-2000.

06-AUG-1999; 99WO-US17915.

10-AUG-1998; 98US-0095960.

(MERI) MERCK & CO INC.

Howard AD, Palyha OC, Smith RG, Tan CP;

WPI: 2000-224272/19.

P-PSDB; AAV69293.

A novel canine growth hormone secretagogue receptor used to identify
 agonists and antagonists -

Claim 2; Fig 1; 32pp; English.

The present sequence encodes a canine growth hormone secretagogue

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2001, 01:48:10 ; Search time 69.99 seconds
(without alignments)
1971.822 Million cell updates/sec

Title: US-09-684-725-1

Perfect score: 729

Sequence: 1 atggaataacttcagatgc.....cactcagagtgtatcag 729

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2_6/plodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/plodata/1/ina/PCrUS.COMB.seq: *
6: /cgn2_6/plodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120.4	16.5	1088	4	US-09-077-675A-6
2	120.4	16.5	1122	4	US-09-077-675A-9
3	114	15.6	1063	4	US-09-077-675A-1
4	112.4	15.4	1029	4	US-09-077-675A-4
5	112.4	15.4	1161	1	US-08-086-439C-2
6	112.4	15.4	1161	1	US-08-434-877-2
7	112.4	15.4	1367	3	US-08-475-742-3
8	112.4	15.4	1370	1	US-08-056-051-1
9	112.4	15.4	1370	1	US-07-928-611-17
10	112.4	15.4	1370	2	US-08-487-811A-17
11	112.4	15.4	1370	4	US-09-060-694-17
12	112.4	15.4	1370	5	PCT-US93-07370-17
13	112.4	15.4	1466	1	US-08-056-051-3
14	112.4	15.4	1466	1	US-07-928-611-19
15	112.4	15.4	1466	2	US-08-487-811A-19
16	112.4	15.4	1466	2	US-09-060-694-19
17	112.4	15.4	1466	5	PCT-US93-07370-19
18	112.4	15.4	1610	1	US-08-056-051-5
19	112.4	15.4	1610	1	US-07-928-611-21
20	112.4	15.4	1610	2	US-08-487-811A-21
21	112.4	15.4	1610	4	US-09-060-694-21
22	112.4	15.4	1610	5	PCT-US93-07370-21
23	110	15.1	1529	3	US-08-858-876A-3
24	109.2	15.0	1092	4	US-09-077-675A-15
25	109.2	15.0	3129	4	US-09-077-675A-14
26	97.6	13.4	1575	3	US-08-858-876A-1
27	88.8	12.2	1601	1	US-08-722-001-7

28	88.8	12.2	1997	1	US-08-722-001-27	Sequence 27, Appl
29	88.8	12.2	2004	1	US-08-722-001-11	Sequence 11, Appl
30	88.6	12.2	1639	1	US-08-334-698-5	Sequence 5, Appl
31	88.6	12.2	1639	1	US-08-228-932-5	Sequence 5, Appl
32	88.6	12.2	1639	1	US-08-468-939-5	Sequence 5, Appl
33	88.6	12.2	1639	2	US-08-406-855A-5	Sequence 5, Appl
34	88.6	12.2	1639	2	US-08-722-190-5	Sequence 5, Appl
35	88.6	12.2	1639	3	US-08-244-354-5	Sequence 5, Appl
36	88.6	12.2	1639	3	US-09-206-899-5	Sequence 5, Appl
37	88.6	12.2	1639	5	PCT-US93-04203-5	Sequence 5, Appl
38	88.4	12.1	836	4	US-09-077-675A-11	Sequence 11, Appl
39	87.6	12.0	1342	3	US-08-832-399-1	Sequence 1, Appl
40	87.6	12.0	1342	4	US-09-372-498-1	Sequence 1, Appl
41	87	11.9	1205	1	US-08-417-103-13	Sequence 13, Appl
42	87	11.9	1634	1	US-07-816-283-1	Sequence 1, Appl
43	87	11.9	1634	1	US-08-417-103-1	Sequence 1, Appl
44	86.8	11.9	921	1	US-08-722-001-17	Sequence 17, Appl
45	86.8	11.9	1567	1	US-08-722-001-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-077-675A-6
Sequence 6, Application US/09077675A
Patent No. 6242199
GENERAL INFORMATION:
APPLICANT: Pal, Lee-Yuh
APPLICANT: Feigner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077, 675A
FILING DATE: 3-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19590P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1088 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
US-09-077-675A-6
Query Match 16.5%; Score 120.4; DB 4; Length 1088;


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QY 252 ggcgggtctctgacccctcgtgctctccttggaatgcgccctggaggtctatgagatg 311
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Db 414 ggccttctccgaactac---tcattctctctgcattgcctccctgcgaactctccgctttg 470
QY 312 ggcgaactacccctctctgttcgggcccgtggtgtctacttcaagaagccctcttga 371
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Db 471 gcagtagcggcccttggaaccttgagcaacctctgtgcaaaccttccagttcgttagcga 530
QY 372 gacgctgtctcgtcctcattccatcagatcacacacgctcagcttgagagcctatgagc 431
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QY 612 caagccatgtggtctacaaattcattcattcaggtacacccctctctacttacttactcct 671
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Db 771 cgtcgcgtccggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 827
QY 672 ccccatgactgactgactgactgactgactgactgactgactgactgactgactgactgact 709
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Db 828 gccgtgtctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 865

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RESULT 5
US-08-439C-2
; Sequence 2, Application US/08086439C
; Patent No. 5468615
; GENERAL INFORMATION:
; APPLICANT: Chio, Christopher L.
; TITLE OF INVENTION: A Synthetic Gene for D4 Dopamine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Upjohn Company, Corp. Intellectual
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,439C
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Darnley Jr., James D.
; REGISTRATION NUMBER: 33,673
; REFERENCE/DOCKET NUMBER: 4700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-385-5210
; TELEFAX: 616-385-6897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-439C-2

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Query Match 15.4%; Score 112.4; DB 1; Length 1161;
Best Local Similarity 53.4%; Pred. 8.2e-16;
Matches 236; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

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QY 139 gtagtgatgagcaatttttgggtgggtggtggtggtggtggtggtggtggtggtggtggt 198
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Db 112 gtgggggggctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 171
QY 199 attctgagacagagatgaaagacagccacacacacacacacacacacacacacacacacac 258
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Db 172 gtggccacagagagagagagagagagagagagagagagagagagagagagagagagagag 231
QY 259 tctgactctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 318
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Db 232 gccgacctctctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 291
QY 319 taccttctgttgcggcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 378
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QY 379 tcttgcctcattcattcattcattcattcattcattcattcattcattcattcattcattc 438
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QY 439 caaccgttcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 498
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Db 412 gtggcgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 471
QY 499 gctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 558
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Db 472 acgtggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 531
QY 559 cactacttcccaatggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 580
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Db 532 gccccgacaccccgccgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 553

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RESULT 6
US-08-434-877-2
; Sequence 2, Application US/08434877
; Patent No. 5721132
; GENERAL INFORMATION:
; APPLICANT: Chio, Christopher L.
; TITLE OF INVENTION: A Synthetic Gene for D4 Dopamine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Upjohn Company, Corp. Intellectual
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette (DS,HD)
; OPERATING SYSTEM: Gateway 2000, p5-90
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,877
; FILING DATE: 1 July 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Darnley Jr., James D.
; REGISTRATION NUMBER: 33,673

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Oy 439 cacccttcgcgcgaacactgcagagcaacccggcgccggaagcctcaagatccttcggcattc 498
Db 518 GTGGCGCGTGCCTACTAACACCGCAGGAGTGGGAGCCGCCGCGACACTGCTCATCGGCGCC 577
Oy 499 gctcggagcttcctccgctgtctcttcctccctgcgaacacaccagatccatgcatcaagtc 558
Db 578 ACGTGCGTGTGTCTCGCGGCGGATGGCGGCCGCTACTGTGTGGCGCTCAACGACGTGGCC 637
Oy 559 cactacttcctcccaatgagtgccc 580
Db 638 GCGCGCGACCCCGCGGTGTGCC 659

RESULT 10
US-08-487-811A-17
: Sequence 17, Application US/08487811A
: Patent No. 5883226
: GENERAL INFORMATION:
: APPLICANT: Clivelli, Olivier
: APPLICANT: Van Tol, Hubert H. M.
: TITLE OF INVENTION: A No. 5883226el Human Dopamine Receptor and Uses
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McDonnell Boehen Hulbert & Berghoff
: STREET: 300 South Wacker Drive
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,811A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5883226nat, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 90,1092-L
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-913-0001
: TELEFAX: 312-913-0002
: TELEX:
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1370 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..103
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: 1268..1370
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 104..1267
: US-08-487-811A-17

Query Match 15.4%; Score 112.4; DB 2; Length 1370;
Best Local Similarity 53.4%; Pred. No. 8.4e-16;
Matches 236; Conservative 0; Mismatches 206; Indels 0; Gaps 0;
Oy 139 ggggggtatgtccaatttgtgtgtgggggtcattgggaagtgcctgtgtgcccgtg 198
Db 218 GTGGGGGGCGTCTCTATCGCGCGGCTGCTCGCGGGAACCTCGCTCTGTGTGCGTGACC 277

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